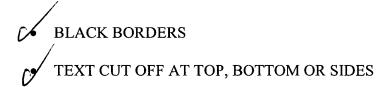
This Page Is Inserted by IFW Operations and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

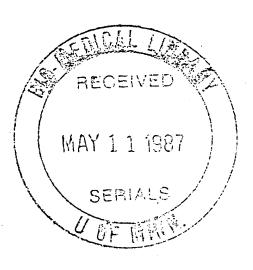


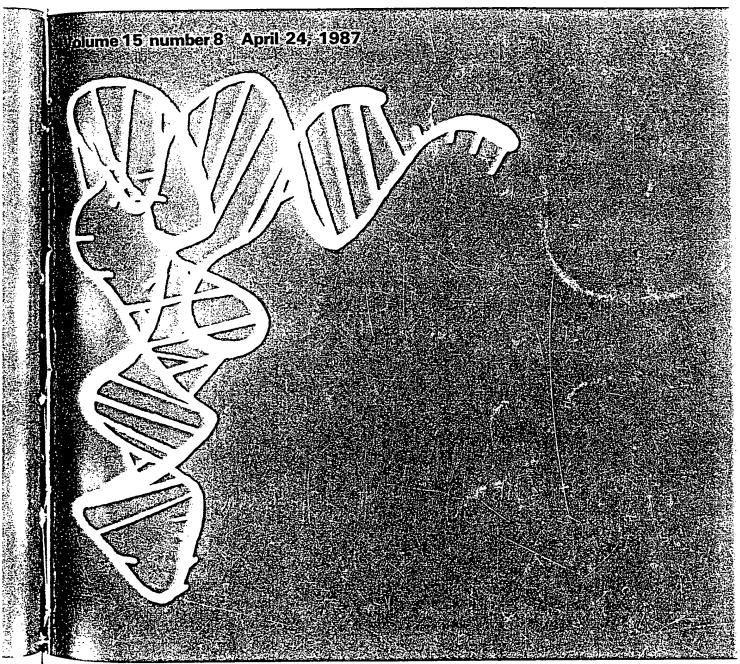
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents will not correct images, please do not report the images to the Image Problem Mailbox.

Nucleic Acids Research







Oxford · Washington DC

ISSN 0305 1048 Coden NARHAD DNA sequences for typical ribosomal gene spacers from Xenopus laevis and Xenopus borealis

* NOTICE: THIS MATERIAL MAY BE PROTECTED BY COPYRIGHT LAW (TITLE 17 U.S. CODE)

Paul Labhart and Ronald H.Reeder

Hutchinson Cancer Research Center, 1124 Columbia Street, Seattle, WA 98104, USA Submitted March 16, 1987

Accession no. Y00132

We have determined a few short DNA sequences that had not been previously reported from the <u>X. laevis</u> ribosomal gene spacer and about 3 kb of previously unreported sequence from the <u>X. borealis</u> spacer. For the convenience of other workers, we have compiled our data with other published reports so that, for the first time, one can refer to a typical, complete sequence for each of these spacers.

For both spacers, the sequence is shown from the C in the HindIIIrecognition site at the 3' end of the 28S rRNA (nucleotide 1) to the
transcription start site of the 40S precursor (X. laevis: at nucleotide 3952;
X. borealis: 3930). The sequence is complied from the following sources: X.
laevis: 1 to 197: (1,2); 190 to 532: (3); 529 to 1474: (2); 1475 to 1664:
present work; 1665 to 2910: (2); 2804 to 3051: (1); 3052 to 3634: inferred
from restriction data in (4); 3635 to 4000: (1,2). X. borealis: 1 to 453:
(3); 454 to 3490: present work; 1081 to 1422: inferred from chemical cleavage
pattern and restriction analysis; 2000 to 2296: inferred from restriction
data; 3385 to 4000: (5). The clones used were pXlr14 in (1,3) and in the
present work, pXl108 in (2,4), and pXbr101A in (5) and in the present work.

						60	70	80	90	108
	10	20	30	49	50			1	1	I.
First nt.		1	1	. 1	1	777777		2227222222	2272828228	CCTTTCCGCG
+1	CTTTT6TC66	AAGGAGCAGG	CCGGAAGGGC	0000000000	CCGGCCGGCG	CONTROL	13175333331	299222227n	CTCTCCCGCA	GGAAGGGGGC
+101	COCCCCACAG	ACCEPTER	136666666666	GHOOCOCCO .	0000-0101		222222222	CCCAPCCCTC .	PERSONAL TO	111111111111111111111111111111111111111
+201	CCAACCCCCC	TTERRETTE	BLALLLLLLL	100010000	000000			CCCACCCCCCC	rerestre e	i bblbllcoc
+301	CACTUTECE	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	LALUULUUUL	CICODOCCCC			22222222	CONTRACTOR A	TELETERITE	PPPLIME
+401	ACCAPGGCCG.	66666666666	BLULULUUUH	OCONCCUNOC			*********	AARGETEGGE	RECUEENIL	LLILLLCOOL
+501	CCCCCTGCCC	RETERREGEE	ALLLILLL	0000117700	0.00000			JUUUUU	CCCAGAGA	TEARGAGGIO
+601	CCTTAAGGGG	regetteett	LAILLLILLL	I BOCCBOOT	MUGHUU IUU		******	ATTATTOOS	GGAGGCAGGG	GAECUGATTU
+701	72222222	CTGAGCCGGG	BLLBLBBBB	BULLUMBOOD	000000.		OCCCCATTCC	CACCCAGGGG	ACCCGATTCG	6661 C6666C
+801	CCCCTTCCCC	ากกรเลยส	GCCCGCTAAG	6000000	000000.000		227742000	CACCCAGGGG	ACCCGATTEG	GGGTCGGGGC
+901	CCCCCCCCCT	CODDDDOOL	CCCCGGGGGGG	LOULTILLE	000100000		ABBCCATTCT	CACCCACCGG	ACCCEATTE	GGGT CGGGGGC
+1001	173333333	0000000000	CCCCGGGGGGG	CGGCTTCCCG	GGGT CCCCCC	EGCGAAGAGA	BBLLLATTE:	CVCLLVCCC	ACCCGATTEG	GGGTCGGGGC
	173333333	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCCGGGGGG	CGGCTTCCCG	GGGTCCCCCC	GGCGAAGAGG	BELLEATER	GHOLLHOOOD	CEATTCERE	TCGGGGCCCC
+1101	CCCCCCCCCCC	CLEGGGGGCCC	CGGGGGGGGGG	CTTCCCGGGG	TCCCCCCCGGC	GAAGAGGGGC	CLATTLIBAD	COMBOOGACC	ATTOGGGGTO	TCGGGGCCCCGG
+1201	CCCCCCCC	ececesecci	CEGGEGCGGC	TCCCGGGCTC	CCCCCGGCGA	AGAGGGGCCC	AT GUUGAUUL	POODONICCO	CCTAGAGAGA	GGGGCCCCGG AGACAGAGGC
+1301	CCCTCCCC	TAAGGGGCC	CGGGGGGGCGG	CTCCCGGGGT	CCCCCCGGCG	AAGAGGGGGG	ANDRUUUAN	DODE DODGED	CELLCLLE	AGACAGAGGC TGAAGAGGGG
+1401	000100000	AAAAAAAT1 1	ACCCCCATE	CCAGCCGGGC	CACCGGGGGG	CCCCCCCCCC	660000000	COAACTICIC	ATRAGGACG	TGAAGAGGGG ATCCGCCCGG
+1501	CCCCCCCCC	C LUTTO COUNTY	CEGAAGAAA	ACCCAGCCGG	GCCACCGGGG	GGCGCCGCGC	ASUBLULL	COACCUTCU	ATECTACEC	ATCCGCCCGG TTTTTGGCAT
+1601	00000000	OTTRAGOTT O	CASGGGCCT	GGGAGAGGAG	CCGGCAGCCC	GECCTETEG	6CCCCCCCGG		ECCLEVICE	TITTIGGCAT G GAGTTCCAGG
+1701	CTCCCCC	DATATAGG	G AGCGGCCTC	CGGGAGCCCT	GECCCEGAAG	TCCCCGCCG	6 666ACCIGG	9 6000000000	COORDITION	G GAGTTCCAGG A GGGGGGGGCAG
+1601	\$16CCGGG	A GEGGGGGG	COCTECTOR A	CTECCTECE	GGGACCTGG	ECCEECCCO	A GCCCCALLG	S GREET LUNCH	ATTTAGGGG	A GGGGGGGGCAG G GGCCGGCCCC
+1901	MOLITOROS	r marritan	A GECEGACES	G GAGTTCCAGO	AGET CGGGC/	GAGGGAGCA	6 SCIEGICE	0.0000000000000000000000000000000000000	CARTTERE	G GGCCGGCCCE C AGAGGGAGCA
+2001	DC TCDTCCC	ATTITION OF	6 GAGETEGGG	C AGGGGGAGCA	A GOCT COT CCI	CCTGCCCTG	CAGCCCGACL	B BEAUTICUA	TOUTOUT ACCUTOOD	C CCCTGCCCTG
+2101	CCCCCCCC	TTTTTTTTTT	C RESESPACET	G GGGACGGCCI	CAGCCCGAC	C GGGAGTTCC	A GGAGCTUGG	6 LAUAUUUHU	T COACCCCO	C CCCTGCCCTG
+2201	99010010	T GCGGACGG	C LLVELLER	C CGGGAGTTC	C AGGAGETEG	g geagaggga	6 CAGGCTCG1	E CCCCIBCCC	COCCUTACI	C CCCCTGCCCT
+2301	COCCOCC	ANDRAGOO 1	TADETORNA R	C CCCCTGCCC	T GCAGCCCGA	C CGGGAGTTC	C AGGAGETCE	G GCAGAGGGA	C TECACCICO	C CCCCTGCCCT A CCGGGAGTTC
+2401	POCCCCO	DIAGGGATGI	C CCCAGCCCG	A CCGGGAGTT	C CAGGAGCTC	g ggcagaggg	A GCAGGCTCE	T CCCCCIGIC	C CACCACCT	A CCGGGAGTTC
+2501	00000000		A ELAGETTE	T CCCCCTGCC	C TGCGGGGGA	C CTGGGCCGC	C CCCAGCCCC	A CCGGGAGII	C CABGAGET	og ggcaggggga og tecegatgag
+ 2601	CAUGADLII	LT CCCCCTEC	T ARRESTRAC	G AAAACCGGG	A GAAATACCC	A GCCGGGCCA	AC COGGGAGGC	C CECGGAGU	C CCCLIGGA	AG TECEGATGAG EG ETGECATGET
• 2701	SACCOST	te terester	ac utreette	A STTCCCAGG	G GCCTGGGGA	g aggagees	SC AGCCCGGCI	7 (7) (6) (6)	C CLBLALGO	CC CCCAGCCCGA
+2801	BALBBATT	TT CCCCCCC	TARRATRA 11	IR TAGGGAGCG	& CETETEGG	A GCCCTGGCI	SC CCAAGTTC	C GCCGGGGA		TT CEAGGAGETE
+2901	ACUCUIT	TO CACCACCT	CC BOCHOSTI	A GRAGGETEE	T CCCCCTGC	C TECEGEGG	ac ctegegec	66 CCCCAGCU	T ACCESSES	TT CCAGGAGCTC CC CTGCGGGGGA
+3001	CLEGGAGI	OF ACCACCUT	CE TOTOTO	T TREAGEE	G ACCEGGAET	T CCAGGAGE	tc GGGCAGAG	GG AGCAGGCT	16 16060016	ADDRESSES SE
+3101	GGGLAGAU	OD ROLADOLI	CO IDECERS	ET TITARGAGE	T CGGGCAGA	SE GAGCAGGC	TC STCCCCCT	BC CCTGCGGG	36 ACCCEBBB	223AA223AA2AAAAAAAAAAAAAAAAAAAAAAAAAAA
+3201	CCCGGGGG	TECACCA	ACTROCOCA	AL REPUBLICATION	T CETCCCCC	TE CCCTECAG	CC CGACCGGG	AG TTCCAGGA	SC TEGGGGAG	AG GGAGCAGGET CT GCCCTGCAGC
+3301	CUACUGGE	PRO (1144669)	CC CAPTIONS	er regrected	GE CCCACCEG	GA STTCCAGG	AG CTCGGGCA	ga gggagcag	SC TUBILUU	CT GCCCTGCAGC GG AGTTCCAGGA
+3401	CETELLL	TO CULTOCOC	AC CTUBERTA	GA GGGAGCAG	GC TCGTCCCC	CT GCCCTGCG	66 GGACCCBG	ee cceecccc	AG CUCCACU	GG AGTTCEAGGA CC GGCACCGGAG
+3501	CUGACUGI	THE DITURDS		or recorrect	AG CCCCACCG	GG AGTTCCAG	GA GCT CGGGC	AG GGGGAGCC	66 CICEICU	20000000000000000000000000000000000000
+3601	6010000	AU AUUUAUU	er cression	TI GCAGATE	CG GCGCCCGC	GG GGACTTGC	TC 66CC666C	CE EECCCCEG	CE SCECCEGG	2222999222 295 2222999222 725
+ 3701	GTCCCCG	DOL CLITTED	TEN CENTERNY	TO BOTTON	CE CCCCEGCC	GG AGTTCCGG	GA GCCCGGGE	iag aggageeg	GC GGCCCGGC	CT CTCGGGCCCC AA AAGGACCGGG
+ 3801	TCCCGCG	LAD BULLIDA	POT BUHCOUNT	TT ECCATETE	CE GECAGGOO	66 TAGGGGA	GA CCGGCCCT	TE ECECGACE	ee ceccce	MA AAGGACCGGG
+3901	CCGCACG	ACG CCTCCATI	DUI MUDUIIII	11 000011010						

FIGURE 1: A typical intergenic spacer region from the ribosomal DNA of Xenopus laevis.

R.G.Snell, I.F.

Molecular Carci University of Ot Submitted Marci

We report he field inversion ge field gel electrop that FIGE gave s ine the possibili strains of C. albi and our ATCC 1 ever, certain sin probes which co Close examinati origins, but havever, we do not 1960 and 1965 Thus, FIGE elec The molecular l interest. Finally

> --=

Figure: Yeast

Lanes a—e are cerevisiae 218 times over the to Ref. 2.

ACKNOWLEDC

We thank I probes, Drs A.

REFERENCES

Carle,G.F.
 Snell,R.G.

First nt. CTTTTGTCCA CTCCCAGAGA AGGAGGAGCA GCGGGGGGG GCGCAAAGAG CCCCCACGGG CGCGGGAACC GTCCCGGTCC GTGACCCTCC GGGGGCCCCCCC CACITAGAC CUTTGGGAL GUGCUCCUT TTCCGCGGGG GGGGAGGGC CCGGGGAGGG CLGGAGGGGG GGAAGGCGC CAGGGGAGGG CACGGGGGAGG CACGGGGAGGC CCGCGGGGAGG CACGCGGGGAGG CACGGGGGAGGA CACGGGGAGGA CACGGGAGGA CACGGGGAGGA CACGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGAGGA CACGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGGAGGA CACGGGAGGA CACGGGGAGGA CACGGGAGGA CACGGGAGGA CACGGAGGAGA CACGGGAGGA CACGGGAGGA CACGGAGGAGA CACGGAGA CACGGAGA CACGGAGGA CACGGAGA CACGAGA CACGGAGA CACGGAGA CACGAGA +101 +201 CCAGGACTTG CCCGGGCGGC CCCCCCCCA CGACCCGCGG AGAAGGGAGC GGGGACCAAG GAGACCAAAC TGTCTGTCCG GCGACGACTT GCCCGCACCC +301 CCGCCGGGG CTGCGGGGCCC GGGGGCCCC GGCGGCCAC GCCACCGGTG GGCCCCCCC GGCGCCCGC CATCGGGCT TAGGGGCCG GGCTTAAGGG CCGGGCTTAA GGGTCGGGC AAGAAAGGG GTCGGGGTAG GGGAGGGTG AGGAAGAGA GAGAAGAGA GAGAAGAGA GAGAAGAGA +501 +601 AGGTTGGGGG CACCTGCTGT AACCCTAACC CTATAGCCCC GACCCGAAAC CTAGCCCTAG CCCTAACCCT AACCCTAACC CTAGCCCTAA CCCTAGCCCT AACCCTAGCC CTAGCCCTAG CCCTAGCCCT AACCCTAGCC CTAGCCCTAG CCCTAGCCCT AACCCTAGCC CTAGCCCTAGCCC AACCCTAGCCC AACCCTAGCCCT AACCCTAGCCT AACCCTAGCCCTAGCCCT AACCCTAGCCCT 4901 +1001 CTARCCCTAR COCTAGOCCT AGOCCCTARCO CTAGOCCTAR COCTAGOCCT AGOCCTARCO CTAGOCCTAR COCTARCOCT AGOCCCTARCO CTAGOCCCTAR +1101 +1201 +1301 CHARCCETA ACCUTANCE CHARCETANCE CTIFECCIAN ACCUTANCE ARCETANCE CHARCCETA ACCUTANCE ARCETANCE CHARCCETANCE CHA +1401 +1501 +1601 +1701 +1801 +1901 42001 COGAGOCICAA AACOGGGACT TUCGUOTTTO GCCACCGGGG GGCCCCCGGG GTGGCCGGGG CGGGGTAGGG GGCTCCCGTG TATTCGGGTT AGGGTTAGGG TTAGGCCCGG GTCGAGCGGA GGCGAAAACG GGGACTTCCG CGTATGGCCA CCGGGGGGCG CCGCGGGCGG GGTAGGGGGC TCCCGTGTAT TAGGGTTAGG •2101 GTTAGGGTTA GRECCGGGTE GAGEGGAGGE SAMALGGGG ACTTCCGCGT TTGGCCACCG GGGGGCGCCG CGGGTGGCGE GRGCGGGGTA GGGGGCTCCC • 2201 GIGTATICES STARGETTA GESTIAGECE CEGGICEAGE GEAGECEANA ACEGEGACTI CECCTITIGE COACCEGEGE ECECCEGES CEGGGIAGES 12301 +2401 +2501 12601 TETGGGGCAE GEAEGAEEGG GGECAELGET GEECGGGCAE GETECGGCAG GAAGGTAGGG ACGAGGTECT CETCALCETG CACCGGCAGE CGEETELGEE • 2701 CGGCCCGGGG TTCCAGGAGC TCGGGCAGGG BAAGCCGGTC CGCCCCTTC CCTCGGAGGG GGCCGAGGCA GCCGCCTCCG CCCGACCGG GGTTCCAGGA BETERGOLAG GOGAAGEEGG TETTEEEEE GAAGTEEGGA CGAGGAEGG CEGGEEGGA GECAGEEGG TETTEGAGGEET ETEGGGGEAE +2601 GEGGGLAGG CGECTCEGET CECEGGGECC GETELGGELAG GAAGGLAGGG GEGAGGECCT CETETCEGG GAALGGAGGE GEAGGLEGGG GEGEGACGTT +3001 +3101 +3201 +3301 +3401 +3501 +3601 +3701 +3801 GETTTTCGGG CACGTGCGGA CAGGGAGGTA GGGAGAGGCC TECTETCGGG GEGCALGGGT CECGAGGEGA GAGGGECGGA GGEEGGGTCA GEEGTCGAGG

FIGURE 2: A typical intergenic spacer region from the ribosomal DNA of Xenopus borealis.

Partial sequences of spacers from other clones can be found in references (6-10). The sequence of the \underline{X} . laevis 40S coding region, up to the 3' end of the 28S sequence, can be assembled from references (7,11,12, and 13).

REFERENCES

- 1. Sollner-Webb, B. and Reeder, R.H. (1979) Cell 18, 485-499.
- 2. Moss, T., Boseley, P.G., and Birnstiel, M.L. (1980) Nucl. Acids Res. 8, 467-485.
- 3. Labhart, P. and Reeder, R.H. (1986) Cell 45, 431-443.
- 4. Boseley, P., Moss, T., Maechler, M., Portmann, R., and Birnstiel, M. (1979) Cell 17, 19-31.
- Furlong, J.C., Forbes, J., Robertson, M., and Maden, B.E.H. (1983) Nucl. Acids Res. 11, 8183-8196.
- Bach, R., Allet, B., and Crippa, M. (1981) Nucl. Acids Res. 9, 5311-5330.
- Maden, B.E.H., Moss, M., and Salim, M. (1982) Nucl. Acids Res. <u>10</u>, 2387-2398.
- 8. LaVolpe, A., Taggart, M., McStay, B., and Bird, A. (1983) Nucl. Acids Res. <u>11</u>,5361-5380.
- 9. McStay, B. and Bird, A. (1983) Nucl. Acids Res. 11, 8167-8181.
- 10. Morgan, G.T., Roan, J.G., Bakken, A.H., and Reeder, R.H. (1984) Nucl. Acids Res. 12, 6043-6052.
- 11. Salim, M., and Maden, B.E.H. (1981) Nature 291, 205-208.
- 12. Hall, L.M.C. and Maden, B.E.H. (1980) Nucl. Acids Res. 8, 5993-6005.
- 13. Ware, V.C., Tague, B.W., Clark, C.G., Gourse, R.L., Brand, R.C., and Gerbi, S.A. (1983) Nucl. Acids Res. 11, 7795-7817.